

SEQUENCE LISTING

<110> Sprecher, Cindy A.
Kisiel, Walter
Foster, Donald C.

<120> NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
METHODS RELATING THERETO

<130> 93-14D4

<150> US 09/904,621
<151> 2001-07-13

<150> US 09/265,627
<151> 1999-03-09

<150> US 08/457,887
<151> 1995-06-01

<150> US 08/147,710
<151> 1993-11-05

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<212> DNA
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<222> (39)...(746)

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1 5

ctg ggg ctg tcg att ctg ctg ctt ttc ctg acg gag gct gca ctg ggc 104
Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly
10 15 20

gat gct gct cag gag cca aca gga aat aac gcg gag atc tgt ctc ctg 152
Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu
25 30 35

ccc cta gac tac gga ccc tgc cgg gcc cta ctt ctc cgt tac tac tac 200
Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr
40 45 50

gac agg tac acg cag agc tgc cgc cag ttc ctg tac ggg ggc tgc gag 248
Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu
55 60 65 70

ggc aac gcc aac aat ttc tac acc tgg gag gct tgc gac gat gct tgc 296
Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys
75 80 85

tgg agg ata gaa aaa gtt ccc aaa gtt tgc cg ^g ctg caa gtg agt gtg Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val 90 95 100	344
gac gac cag tgt gag ggg tcc aca gaa aag tat ttc ttt aat cta agt Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser 105 110 115	392
tcc atg aca tgt gaa aaa ttc ttt tcc ggt ggg tgt cac cg ^g aac cg ^g Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg 120 125 130	440
att gag aac agg ttt cca gat gaa gct act tgt atg ggc ttc tgc gca Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala 135 140 145 150	488
cca aag aaa att cca tca ttt tgc tac agt cca aaa gat gag gga ctg Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu 155 160 165	536
tgc tct gcc aat gtg act cgc tat tat ttt aat cca aga tac aga acc Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr 170 175 180	584
tgt gat gct ttc acc tat act ggc tgt gga ggg aat gac aat aac ttt Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Asn Asp Asn Asn Phe 185 190 195	632
gtt agc agg gag gat tgc aaa cgt gca tgt gca aaa gct ttg aaa aag Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys 200 205 210	680
aaa aag aag atg cca aag ctt cgc ttt gcc agt aga atc cg ^g aaa att Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile 215 220 225 230	728
cg ^g aag aag caa ttt taa acattcttaa tatgtcatct tg ^{ttt} gtctt Arg Lys Lys Gln Phe * 235	776
tatggcttat ttgcctttat gg ^{tt} gtatct gaagaataat atgacagcat gag ^{ggaa} acaa 836 atcat ^{tt} ggtg atttattcac cag ^{tttt} at taatacaagt cactttca aaaatttgg 896 ttttttata tataactagc tgctattcaa atgtgagtct accat ^{tttta} atttatgg 956 caactgtttg tgagactgaa ttc 979	
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Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu 35 40 45	
Leu Leu Arg Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe 50 55 60	
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu 65 70 75 80	
Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys	

85	90	95
Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys		
100	105	110
Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly		
115	120	125
Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr		
130	135	140
Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser		
145	150	155
Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe		
165	170	175
Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly		
180	185	190
Gly Asn Asp Asn Asn Phe Val Ser Arg Glu Asp Cys Lys Arg Ala Cys		
195	200	205
Ala Lys Ala Leu Lys Lys Lys Lys Lys Met Pro Lys Leu Arg Phe Ala		
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Ser Arg Ile Arg Lys Ile Arg Lys Lys Gln Phe		
225	230	235

<210> 3
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<222> (77) ... (235)

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Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly
1 5 10

ttc tgc tgg gcc caa cca gtc act ggc gat gaa tca tct gtt gag att 160
Phe Cys Trp Ala Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile
15 20 25

ccg gaa gag tct ctg atc atc gct gaa aac acc act ttg gct aac gtc 208
Pro Glu Glu Ser Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val
30 35 40

gcc atg gct gag aga ttg gag aag aga 235
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45 50

<210> 8
<211> 53
<212> PRT
<213> Homo sapiens

<400> 8
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Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
20 25 30
Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
35 40 45
Arg Leu Glu Lys Arg
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<210> 9
<211> 17
<212> DNA
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<220>
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<400> 9
gtaaaacgac ggccagt 17

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<223> NOR-2523

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<210> 11
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<212> DNA
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<223> M-2162

<400> 11
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<210> 13
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal

<400> 13
Ala Gln Glu Pro Thr Gly Asn Asn
 1           5

<210> 14
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<212> DNA
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<220>
<221> variation
<222> (0)...(0)
<223> Kunitz domain

<221> variation
<222> (1)...(3)
<223> Codon-1 Wherein the nucleotide triplet 1-3
      encodes any amino acid except cysteine.

<221> variation
<222> (4)...(6)
<223> Codon-2 Wherein the nucleotide triplet 4-6

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